

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 3, 2005, 21:37:29 / Search time 52.7808 Seconds

(without alignments)
291.060 Million cell updates/sec

Title: 09782816-1-22
Perfect score: 138
Sequence: 1 EYEKIKTVKESATEBKLTPLVLAQKOLAL 30

$X=0$
 $X=1$
 $X=2$
 $X=3$

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: UniProt 03:1
1: uniprot_sprot:1
2: uniprot_trembl:1

Pred. No. is the number of results predicted to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	138	100.0	400	1 DCT2_HUMAN	013561 homo sapien
2	135	97.8	401	1 DCT2_MOUSE	099fj8 mus musculu
3	135	97.8	402	1 Q6A1H5	06ayh5 rattus norv
4	114	82.6	338	2 Q7ZXY2	07zxy2 xenopus lae
5	114	82.6	403	2 Q6IRB3	06irb3 xenopus lae
6	109	79.0	403	2 Q66J30	066j30 xenopus lae
7	92	66.7	405	2 Q7J3H1	07j3h1 brachydanio
8	89	64.5	402	2 Q9PTG6	09ptg6 gallus gall
9	56	40.6	333	2 Q874B7	0874b7 paecilomyce
10	54	39.1	445	2 Q7ZJL4	07zjl4 thermus the
11	54	39.1	500	1 C72Y ARATH	072y arath
12	54	39.1	769	2 Q6BPD3	06bpd3 arabidopsis
13	54	39.1	933	1 G1AND ACOBR	08qdt1 azospirillum
14	53	38.4	416	2 Q6BFF2	06bff2 parametium
15	53	38.4	710	2 Q6CE32	06c32 yarrowia 11
16	53	38.4	1373	2 Q75CZ5	075cz5 ashbya gos
17	53	38.4	1773	2 Q01787	001787 caenorhabdi
18	52	37.7	449	2 Q738U0	0738u0 bacillus ce
19	52	37.7	452	2 Q81DX2	081dx2 bacillus ce
20	52	37.7	470	2 Q6FAP3	06fap3 acinetobact
21	52	37.7	1330	2 Q7RT55	07rt55 plasmodium
22	51	37.0	131	2 Q81T25	081t25 pyrococcus
23	51	37.0	23	2 Q25636	025636 parechnus
24	51	37.0	319	2 Q8P818	08p818 methanosarc
25	51	37.0	378	2 Q6UYC7	06uyc7 actinobacill
26	51	37.0	389	2 Q8KRB8	08krb8 helicobacte
27	51	37.0	389	2 Q8LON4	08lon4 helicobacte
28	51	37.0	389	2 Q8LON6	08lon6 helicobacte
29	51	37.0	389	2 Q8LON9	08lon9 helicobacte
30	51	37.0	389	2 Q8LOP0	08lop0 helicobacte
31	51	37.0	389	2 Q8LOP1	08lop1 helicobacte

32	51	37.0	389	2 Q8LOP2	08lop2 helicobacte
33	51	37.0	389	2 Q8LOP5	08lop5 helicobacte
34	51	37.0	389	2 Q8LOP7	08lop7 helicobacte
35	51	37.0	500	1 C72V ARATH	072v arath
36	51	37.0	757	2 Q96WU0	096wu0 arabidopsis
37	51	37.0	770	2 Q7ZF42	07zf42 desulfocib
38	51	37.0	773	1 GYRB HELPU	09z1k3 helicobacte
39	51	37.0	928	2 Q660E1	0660e1 borrelia ga
40	51	37.0	932	2 Q51674	051674 borrelia bu
41	51	37.0	964	1 IF2_CHEVO	051674 borrelia bu
42	51	37.0	10917	2 Q93NM6	093nm6 streptomyce
43	50.5	36.6	213	1 LIBB_SALTY	08zr03 salmonella
44	50.5	36.6	213	1 LIBB_SALTY	08zr03 salmonella
45	50.5	36.6	380	2 Q7MPU5	07mpu5 vibrio vuln

ALIGNMENTS

RESULT 1
DCT2_HUMAN STANDARD; PRT; 400 AA.
AC Q13561; Q86Y2; Q9BW17;
DT 01-NOV-1997 (Rel. 35, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Dynactin complex 50 kDa subunit (50 kDa dynein-associated polypeptide)
DB (p50 dynactin) (DCTN-50) (Dynactin 2).
GN Name=DCTN2; Synonyms=DCTN50;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=96178072; PubMed=8647893; DOI=10.1093/jcb.132.4.617;
RA Echeverri C.J., Paschal B.M., Vaughan K.T., Vallee R.B.;
RT "Molecular characterization of the 50-kD subunit of dynactin reveals
RT organization for the complex in chromosome alignment and spindle
RT J. Cell Biol. 132:617-633(1996)."
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta, Skin, and Uterus;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Rappaport J., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stappleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lonnellano N.A., Peters K.J., Abramson R.D., Millar J.S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Guaratine P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallal D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield V.S.N., Krzywicki M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE OF 1-384 FROM N.A.
RA Aumais J.P., Yu-Lee U.-Y.;
RT "Human 50 kD dynactin subunit, p50 dynactin, isolated from HeLa
RT cells.";
RN Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-13.

Exhibit 3

10A

Exhibit 3
2 of 2

RC TISSUE=platelet; PubMed=12665801; DOI=10.1038/nbr810;
RX MEDLINE=22608298; Goehals M., Martens L., Van Damme J., Staes A.,
RA Gevaert K., Vandekerckhove J.,
RT "Exploring proteomes and analyzing protein processing by mass
RT spectrometric identification of sorted N-terminal peptides.";
RL Nat. Biotechnol. 21:566-569(2003)
CC -1- FUNCTION: Modulates cytoplasmic dynein binding to an organelle,
CC and plays a role in prometaphase chromosome alignment and spindle
CC organization during mitosis. May play a role in synapse formation
CC during brain development.
CC -1- SUBUNIT: Subunit of dynein, a multiprotein complex associated
CC with dynein.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated.
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
DR EMBL; U50733; AAC05423.1; -
DR EMBL; BC000718; AA000718.1; -
DR EMBL; BC009468; AA009468.1; -
DR EMBL; BC014083; AA014083.1; -
DR EMBL; AY189155; AA034395.1; -
DR Genbank; HGNC:2712; DCTN2.
DR MTM; 607376; -
DR GO; GO:0005813; C:centrosome; TAS.
DR GO; GO:0005869; C:dynactin complex; TAS.
DR GO; GO:0000776; C:kinetochore; TAS.
DR GO; GO:0008283; P:cell proliferation; TAS.
DR GO; GO:0007067; P:mitosis; TAS.
DR InterPro; IPR006996; Dynactin.
DR Pfam; PF04912; Dynactin; 1.
DR Collied coil; Cytokeleton; Direct protein sequencing; Dynein;
KW Membrane; Microtubule; Motor protein.
FT INIT MET 0
FT DOMAIN 98 131 Coiled coil (Potential).
FT DOMAIN 213 243 Coiled coil (Potential).
FT DOMAIN 378 398 Coiled coil (Potential).
FT COMFLICT 34 34 A -> AFAGEL (in Ref. 1).
FT COMFLICT 35 35 A -> ELK (in Ref. 3).
FT COMFLICT 384 384 LATV -> PGHS (in Ref. 3).
SQ SEQUENCE 400 AA; 44099 MW; 0A05A595C0B8270F CRC64;
Query Match Best Local Similarity 100.0%; Score 138; DB 1; Length 400;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DY 1 EEEKIKTVKESATEKLTPLAKOLAAL 30
DB 115 EEEKIKTVKESATEKLTPLAKOLAAL 144
RESULT 2
DCTN2_MOUSE STANDARD; PRT; 401 AA.
AC Q99KJ8; 28-FEB-2003 (Rel. 41, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Dynactin complex 50 kDa subunit (50 kDa dynein-associated polypeptide)
DE (p50 dynactin) (DCTN-50) (Dynactin 2) (Growth cone membrane protein
DE 23-48k) (GMP23-48k).
GN Name=Dctn2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins B.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
RA Altschuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.L., Wang J., Hsieh F.,
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.B.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Young A.C., Rodriguez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Diatchenko G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
RA Buterfield Y.S.N., Krzywinski M.T., Skalska U., Smallus D.B.,
RA Scherch A., Schein J.E., Jones S.J.W., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RL [2]
RP SEQUENCE OF 65-74; 77-91; 102-116; 156-170; 194-216 AND 309-320,
RP SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
RP TISSUE=Brain.
RX MEDLINE=97288622; PubMed=9144527; DOI=10.1006/dbrc.1997.6447;
RA Abe T.K., Tanaka H., Iwanaga T., Odani S., Kuwano R.,
RT "The presence of the 50-kDa subunit of dynein complex in the nerve
RT growth cone.";
RL Biochem. Biophys. Res. Commun. 233:295-299(1997).
RL [3]
RP INTERACTION WITH BICD2.
RX MEDLINE=21376052; PubMed=11483508; DOI=10.1093/emboj/20.15.4041;
RA Hoogenraad C.C., Akhmanova A., Howell S.A., Dordland B.R.,
RA de Zeeuw C.I., Willemsen R., Visser P., Grosved F., Galjart N.,
RT "Mammalian Golgi-associated Bicaudal-2 functions in the dynein-
RT dynein pathway by interacting with these complexes.";
RL EMBL J. 20:4041-4054(2001).
CC -1- FUNCTION: Modulates cytoplasmic dynein binding to an organelle,
CC and plays a role in prometaphase chromosome alignment and spindle
CC organization during mitosis. May play a role in synapse formation
CC during brain development.
CC -1- SUBUNIT: Subunit of dynein, a multiprotein complex associated
CC with dynein (by similarity). Interacts with BICD2.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated.
CC and membrane-associated forms in neonates. Levels of membrane-
CC associated form are greatly reduced in the adult.
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CC or send an email to license@isb-sib.ch).
DR EMBL; BC004613; AA004613.1; -
DR MGD; MG1:107733; Dctn2.
DR InterPro; IPR006996; Dynactin.
DR Pfam; PF04912; Dynactin; 1.
KW Coiled coil; Cytokeleton; Direct protein sequencing; Dynein;
KW Membrane; Microtubule; Motor protein.
FT INIT MET 0
FT DOMAIN 98 131 Coiled coil (Potential).
FT DOMAIN 214 244 Coiled coil (Potential).
SQ SEQUENCE 401 AA; 43985 MW; 1535BAABD5940EBC CRC64;
Query Match Best Local Similarity 97.8%; Score 135; DB 1; Length 401;
Matches 29; Conservative 1; Mismatches 0; Indels 0; Gaps 0;